



Substitute 47113.txt

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Therion, Corporation
- (ii) TITLE OF THE INVENTION: Recombinant Pox Virus For  
Immunization Against MUC1 Tumor-Associated Antigen
- (iii) NUMBER OF SEQUENCES: 21
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: NIXON PEABODY LLP
  - (B) STREET: 100 Summer Street
  - (C) CITY: Boston
  - (D) STATE: MA
  - (E) COUNTRY: USA
  - (F) ZIP: 02110-2131
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 10/057,136
  - (B) FILING DATE: 25-JAN-2002
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 09/366,670
  - (B) FILING DATE: 03-AUG-1999
  - (C) CLASSIFICATION:
- (viii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: PCT/US98/03693
  - (B) FILING DATE: 24-FEB-1998
  - (C) CLASSIFICATION:
- (ix) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 60/038,253
  - (B) FILING DATE: 24-FEB-1997
- (x) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Eisenstein, Ronald I
  - (B) REGISTRATION NUMBER: 30,628
  - (C) REFERENCE/DOCKET NUMBER: 700953-047113-C2-RCE
- (xi) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 617-345-6054
  - (B) TELEFAX: 617-345-1300
  - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr  
 1 5 10 15  
 Arg Pro Ala Pro  
 20

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGCTCCACCG CCCCCCAGC CCACGGTGTC ACCTCGGCCC CGGACACCAG GCCGGCCCCG 60

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Pro Asp Thr Arg Pro Ala Pro  
 1 5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGCAGTACTG CACCACCGGC ACATGGCGTA ACATCAGCAC CTGATACAAG ACCTGCACCT 60

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGATCCACCG CGCCGCCTGC GCACGGAGTG ACGTCGGCGC CCGACACGCG CCCCCTCCC 60

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGGTCAACAG CTCCTCCCGC TCATGGGGTT ACTTCTGCTC CAGATACTCG CCCAGCTCCA 60

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGTTCGACGG CCCCCCTGC TCACGGTGTA ACATCCGCCC CGGATACCAG ACCGGCCCCT 60

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGCAGCACCG CACCGCCCGC ACACGGGGTC ACAAGCGCGC CAGACACTCG ACCTGCGCCA 60

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGAAGTACCG CTCCACCTGC ACACGGGGTC ACAAGCGCGC CAGACACTCG ACCTGCGCCA 60

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGTCGACTG CCCCTCCGGC GCATGGTGTG ACCTCAGCTC CTGACACAAG GCCAGCCCCA 60

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGTTCAACGG CACCTCCAGC ACACGGAGTC ACGTCTGCAC CCGACACCCG TCCAGCTCCG 60

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGTAGTACAG CGCCACCCGC ACATGGCGTC ACGAGCGCTC CGGATACGAG ACCGGCGCCT 60

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGCTCCACCG CACCCCCAGC CCACGGTGTC ACCTCGGCCC CGGACACCAG GCGGGCCCCG 60  
GGCTCCACCC CGGCCCGG 78

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGCTCCACCG CCCCCCAGC CCATGGTGTG ACCTCGGCCC CGGACAACAG GCCCGCCTTG 60

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGCTCCACCG CCCCTCCAGT CCACAATGTC ACCTCGGCC

39

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr
1				5				10						15	
Arg	Arg	Ala	Pro												
			20												

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Asn
1				5				10						15	
Arg	Pro	Ala	Leu												
			20												

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gly	Ser	Thr	Ala	Pro	Pro	Val	His	Asn	Val	Thr	Ser	Ala
1				5				10				

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1524

## (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATG Met 1	ACA Thr	CCG Pro	GGC Gly	ACC Thr 5	CAG Gln	TCT Ser	CCT Pro	TTC Phe 10	TTC Phe	CTG Leu	CTG Leu	CTG Leu	CTC Leu 15	CTC Leu	ACA Thr	48
GTG Val	CTT Leu	ACA Thr	GCT Ala 20	ACC Thr	ACA Thr	GCC Ala	CCT Pro	AAA Lys 25	CCC Pro	GCA Ala	ACA Thr	GTT Val 30	GTT Val	ACG Thr	GGT Gly	96
TCT Ser	GGT Gly	CAT His 35	GCA Ala	AGC Ser	TCT Ser	ACC Thr	CCA Pro 40	GGT Gly	GGA Gly	GAA Glu	AAG Lys	GAG Glu 45	ACT Thr	TCG Ser	GCT Ala	144
ACC Thr	CAG Gln 50	AGA Arg	AGT Ser	TCA Ser	GTG Val	CCC Pro 55	AGC Ser	TCT Ser	ACT Thr	GAG Glu	AAG Lys 60	AAT Asn	GCT Ala	GTG Val	AGT Ser	192
ATG Met 65	ACA Thr	AGC Ser	TTG Leu	ATA Ile	TCG Ser 70	AAT Asn	TCC Ser	GGT Gly	GTC Val	CGG Arg 75	GGC Gly	TCC Ser	ACC Thr	GCC Ala	CCC Pro 80	240
CCA Pro	GCC Ala	CAC His	GGT Gly	GTC Val 85	ACC Thr	TCG Ser	GCC Ala	CCG Pro	GAC Asp 90	ACC Thr	AGG Arg	CCG Pro	GCC Ala	CCG Pro 95	GGC Gly	288
TCC Ser	ACC Thr	GCC Ala	CCC Pro 100	CCA Pro	GCC Ala	CAC His	GGT Gly	GTC Val 105	ACC Thr	TCG Ser	GCC Ala	CCG Pro	GAC Asp 110	ACC Thr	AGG Arg	336
CCG Pro	GCC Ala	CCG Pro 115	GGC Gly	TCC Ser	ACC Thr	GCC Ala	CCC Pro 120	CCA Pro	GCC Ala	CAC His	GGT Gly	GTC Val 125	ACC Thr	TCG Ser	GCC Ala	384
CCG Pro	GAC Asp 130	ACC Thr	AGG Arg	CCG Pro	GCC Ala	CCG Pro 135	GGC Gly	TCC Ser	ACC Thr	GCA Ala	CCC Pro 140	CCA Pro	GCC Ala	CAC His	GGT Gly	432
GTC Val 145	ACC Thr	TCG Ser	GCC Ala	CCG Pro	GAC Asp 150	ACC Thr	AGG Arg	CGG Arg	GCC Ala	CCG Pro 155	GGC Gly	TCC Ser	ACC Thr	CCG Pro	GCC Ala 160	480
CCG Pro	GGC Gly	TCC Ser	ACC Thr	GCC Ala 165	CCC Pro	CCA Pro	GCC Ala	CAC His	GGT Gly 170	GTC Val	ACC Thr	TCG Ser	GCC Ala	CCG Pro 175	GAC Asp	528
ACC Thr	AGG Arg	CCG Pro	GCC Ala 180	CCG Pro	GGC Gly	TCC Ser	ACC Thr	GCC Ala 185	CCC Pro	CCA Pro	GCC Ala	CAT His	GGT Gly 190	GTC Val	ACC Thr	576
TCG Ser	GCC Ala	CCG Pro 195	GAC Asp	AAC Asn	AGG Arg	CCC Pro	GCC Ala 200	TTG Leu	GGC Gly	TCC Ser	ACC Thr	GCC Ala 205	CCT Pro	CCA Pro	GTC Val	624
CAC His 210	AAT Asn	GTC Val	ACC Thr	TCG Ser	GCC Ala	TCA Ser 215	GGC Gly	TCT Ser	GCA Ala	TCA Ser	GGC Gly 220	TCA Ser	GCT Ala	TCT Ser	ACT Thr	672
CTG Leu	GTG Val	CAC His	AAC Asn	GGC Gly	ACC Thr	TCT Ser	GCC Ala	AGG Arg	GCT Ala	ACC Thr	ACA Thr	ACC Thr	CCA Pro	GCC Ala	AGC Ser	720

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225				230				235				240				
AAG Lys	AGC Ser	ACT Thr	CCA Pro	TTC Phe 245	TCA Ser	ATT Ile	CCC Pro	AGC Ser	CAC His 250	CAC His	TCT Ser	GAT Asp	ACT Thr	CCT Pro 255	ACC Thr	768
ACC Thr	CTT Leu	GCC Ala	AGC Ser 260	CAT His	AGC Ser	ACC Thr	AAG Lys	ACT Thr 265	GAT Asp	GCC Ala	AGT Ser	AGC Ser	ACT Thr 270	CAC His	CAT His	816
AGC Ser	ACG Thr	GTA Val 275	CCT Pro	CCT Pro	CTC Leu	ACC Thr	TCC Ser 280	TCC Ser	AAT Asn	CAC His	AGC Ser	ACT Thr 285	TCT Ser	CCC Pro	CAG Gln	864
TTG Leu	TCT Ser 290	ACT Thr	GGG Gly	GTC Val	TCT Ser	TTC Phe 295	TTT Phe	TTC Phe	CTG Leu	TCT Ser	TTT Phe 300	CAC His	ATT Ile	TCA Ser	AAC Asn	912
CTC Leu 305	CAG Gln	TTT Phe	CCT Pro	TCC Ser	TCT Ser 310	CTC Leu	GAA Glu	GAT Asp	CCC Pro	AGC Ser 315	ACC Thr	GAC Asp	TAC Tyr	TAC Tyr	CAA Gln 320	960
GAG Glu	CTG Leu	CAG Gln	AGA Arg	GAC Asp 325	ATT Ile	TCT Ser	CAA Gln	ATG Met	TTT Phe 330	TTG Leu	CAG Gln	ATT Ile	TAT Tyr	AAA Lys 335	CAA Gln	1008
GGG Gly	GGT Gly	TTT Phe	CTG Leu 340	GGC Gly	CTC Leu	TCC Ser	AAT Asn	ATT Ile 345	AAG Lys	TTC Phe	AGG Arg	CCA Pro	GGA Gly 350	TCT Ser	GTG Val	1056
CTG Leu	GTA Val 355	CAA Gln	TTG Leu	ACT Thr	CTG Leu	GCC Ala	TTC Phe 360	CGA Arg	GAA Glu	GGT Gly	ACC Thr	ATC Ile 365	AAT Asn	GTC Val	CAC His	1104
GAC Asp	GTG Val 370	GAG Glu	ACA Thr	CAG Gln	TTC Phe	AAT Asn 375	CAG Gln	TAT Tyr	AAA Lys	ACG Thr	GAA Glu 380	GCA Ala	GCC Ala	TCT Ser	CGA Arg	1152
TAT Tyr 385	AAC Asn	CTG Leu	ACG Thr	ATC Ile	CCA Pro 390	GAC Asp	GTC Val	AGC Ser	GTG Val	AGT Ser 395	GAT Asp	GTG Val	CCA Pro	TTT Phe	CCT Pro 400	1200
TTC Phe	TCT Ser	GCC Ala	CAG Gln	TCT Ser 405	GGG Gly	GCT Ala	GGG Gly	GTG Val	CCA Pro 410	GGC Gly	TGG Trp	GGC Gly	ATC Ile	GCG Ala 415	CTG Leu	1248
CTC Leu	CTG Leu	CTG Leu	GTC Val 420	TGT Cys	GTT Val	CTG Leu	GTT Val	GCG Ala 425	CTG Leu	GCC Ala	ATT Ile	GTC Val	TAT Tyr 430	CTC Leu	ATT Ile	1296
GCC Ala	TTG Leu	GCT Ala 435	GTC Val	TGT Cys	CAG Gln	TGC Cys	CGC Arg 440	CGA Arg	AAG Lys	AAC Asn	TAC Tyr	GGG Gly 445	CAG Gln	CTG Leu	GAC Asp	1344
ATC Ile	TTT Phe 450	CCA Pro	GCC Ala	CGG Arg	GAT Asp	ACC Thr 455	TAC Tyr	CAT His	CCT Pro	ATG Met	AGC Ser 460	GAG Glu	TAC Tyr	CCC Pro	ACC Thr	1392
TAC Tyr 465	CAC His	ACC Thr	CAT His	GGG Gly	CGC Arg 470	TAT Tyr	GTC Val	CCC Pro	CCT Pro	AGC Ser 475	AGT Ser	ACC Thr	GAT Asp	CGT Arg	AGC Ser 480	1440
CCC	TAT	GAG	AAG	GTT	TCT	GCA	GGT	AAT	GGT	GGC	AGC	AGC	CTC	TCT	TAC	1488

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Pro	Tyr	Glu	Lys	Val	Ser	Ala	Gly	Asn	Gly	Gly	Ser	Ser	Leu	Ser	Tyr
				485					490					495	

ACA	AAC	CCA	GCA	GTG	GCA	GCC	ACT	TCT	GCC	AAC	TTG	TAG
Thr	Asn	Pro	Ala	Val	Ala	Ala	Thr	Ser	Ala	Asn	Leu	
			500					505				

1527

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met	Thr	Pro	Gly	Thr	Gln	Ser	Pro	Phe	Phe	Leu	Leu	Leu	Leu	Leu	Thr
1				5				10						15	
Val	Leu	Thr	Ala	Thr	Thr	Ala	Pro	Lys	Pro	Ala	Thr	Val	Val	Thr	Gly
			20					25					30		
Ser	Gly	His	Ala	Ser	Ser	Thr	Pro	Gly	Gly	Glu	Lys	Glu	Thr	Ser	Ala
		35					40					45			
Thr	Gln	Arg	Ser	Ser	Val	Pro	Ser	Ser	Thr	Glu	Lys	Asn	Ala	Val	Ser
	50					55					60				
Met	Thr	Ser	Leu	Ile	Ser	Asn	Ser	Gly	Val	Arg	Gly	Ser	Thr	Ala	Pro
65					70					75					80
Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly
			85						90					95	
Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg
			100					105					110		
Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala
		115					120					125			
Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly
	130					135					140				
Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Arg	Ala	Pro	Gly	Ser	Thr	Pro	Ala
145					150					155					160
Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp
				165					170					175	
Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr
			180					185					190		
Ser	Ala	Pro	Asp	Asn	Arg	Pro	Ala	Leu	Gly	Ser	Thr	Ala	Pro	Pro	Val
		195					200					205			
His	Asn	Val	Thr	Ser	Ala	Ser	Gly	Ser	Ala	Ser	Gly	Ser	Ala	Ser	Thr
	210					215					220				
Leu	Val	His	Asn	Gly	Thr	Ser	Ala	Arg	Ala	Thr	Thr	Thr	Pro	Ala	Ser
225					230					235					240
Lys	Ser	Thr	Pro	Phe	Ser	Ile	Pro	Ser	His	His	Ser	Asp	Thr	Pro	Thr
				245					250					255	
Thr	Leu	Ala	Ser	His	Ser	Thr	Lys	Thr	Asp	Ala	Ser	Ser	Thr	His	His
			260					265					270		
Ser	Thr	Val	Pro	Pro	Leu	Thr	Ser	Ser	Asn	His	Ser	Thr	Ser	Pro	Gln
		275					280					285			
Leu	Ser	Thr	Gly	Val	Ser	Phe	Phe	Phe	Leu	Ser	Phe	His	Ile	Ser	Asn
	290					295					300				
Leu	Gln	Phe	Pro	Ser	Ser	Leu	Glu	Asp	Pro	Ser	Thr	Asp	Tyr	Tyr	Gln
305					310					315					320
Glu	Leu	Gln	Arg	Asp	Ile	Ser	Gln	Met	Phe	Leu	Gln	Ile	Tyr	Lys	Gln
				325					330					335	



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Gly	Gly	Phe	Leu	Gly	Leu	Ser	Asn	Ile	Lys	Phe	Arg	Pro	Gly	Ser	Val
			340					345					350		
Leu	Val	Gln	Leu	Thr	Leu	Ala	Phe	Arg	Glu	Gly	Thr	Ile	Asn	Val	His
		355					360					365			
Asp	Val	Glu	Thr	Gln	Phe	Asn	Gln	Tyr	Lys	Thr	Glu	Ala	Ala	Ser	Arg
		370				375					380				
Tyr	Asn	Leu	Thr	Ile	Pro	Asp	Val	Ser	Val	Ser	Asp	Val	Pro	Phe	Pro
385					390					395					400
Phe	Ser	Ala	Gln	Ser	Gly	Ala	Gly	Val	Pro	Gly	Trp	Gly	Ile	Ala	Leu
			405						410					415	
Leu	Leu	Leu	Val	Cys	Val	Leu	Val	Ala	Leu	Ala	Ile	Val	Tyr	Leu	Ile
			420					425					430		
Ala	Leu	Ala	Val	Cys	Gln	Cys	Arg	Arg	Lys	Asn	Tyr	Gly	Gln	Leu	Asp
		435					440					445			
Ile	Phe	Pro	Ala	Arg	Asp	Thr	Tyr	His	Pro	Met	Ser	Glu	Tyr	Pro	Thr
		450				455					460				
Tyr	His	Thr	His	Gly	Arg	Tyr	Val	Pro	Pro	Ser	Ser	Thr	Asp	Arg	Ser
465					470					475					480
Pro	Tyr	Glu	Lys	Val	Ser	Ala	Gly	Asn	Gly	Gly	Ser	Ser	Leu	Ser	Tyr
			485					490						495	
Thr	Asn	Pro	Ala	Val	Ala	Ala	Thr	Ser	Ala	Asn	Leu				
			500					505							

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Gly	Ser	Thr	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr
1				5					10					15		
Ser	Ala	Phe	Asp	Thr	Arg	Pro	Ala	Pro								
		20				25										